

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hermeking, Heiko  
Vogelstein, Bert  
Kinzler, Kenneth
- (ii) TITLE OF THE INVENTION: 14-3-3 SIGMA ARREST THE CELL  
CYCLE
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Banner & Witcoff
  - (B) STREET: 1001 G Street, NW
  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20001
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 18-DEC-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Kagan, Sarah A
  - (B) REGISTRATION NUMBER: 32141
  - (C) REFERENCE/DOCKET NUMBER: 1107.72886
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 202-508-9100
  - (B) TELEFAX: 202-508-9299
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGAGACACA	GAGTCCGGCA	TTGGTCCCAG	GCAGCAGTTA	GCCCGCCGCC	CGCCTGTGTG	60
TCCCCAGAGC	CATGGAGAGA	GCCAGTCTGA	TCCAGAAGGC	CAAGCTGGCA	GAGCAGGCCG	120
AACGCTATGA	GGACATGGCA	GCCTTCATGA	AAGGCGCCGT	GGAGAAGGGC	GAGGAGCTCT	180
CCTGCGAAGA	GCGAAACCTG	CTCTCAGTAG	CCTATAAGAA	CGTGGTGGGC	GGCCAGAGGG	240
CTGCCTGGAG	GGTGCTGTCC	AGTATTGAGC	AGAAAAGCAA	CGAGGAGGGC	TCGGAGGAGA	300
AGGGGCCCGA	GGTGCCTGAG	TACCGGGAGA	AGGTGGAGAC	TGAGCTCCAG	GGCGTGTGCG	360
ACACCGTGCT	GGGCCTGCTG	GACAGCCACC	TCATCAAGGA	GGCCGGGGAC	GCCGAGAGCC	420
GGGTCTTCTA	CCTGAAGATG	AAGGGTGACT	ACTACCGCTA	CCTGGCCGAG	GTGGCCACCG	480
GTGACGACAA	GAAGCGCATC	ATTGACTCAG	CCCGGTCAGC	CTACCAGGAG	GCCATGGACA	540
TCAGCAAGAA	GGAGATGCCG	CCCACCAACC	CCATCCGCTT	GGGCCTGGCC	CTGAACCTTT	600
CCGTCTTCCA	CTACGAGATC	GCCAACAGCC	CCGAGGAGGC	CATCTCTCTG	GCCAAGACCA	660
CTTTTCGACGA	GGCCATGGCT	GATCTGCACA	CCCTCAGCGA	GGACTCCTAC	AAAGACAGCA	720
CCCTCATCAT	GCAGCTGCTG	CGAGACAACC	TGACACTGTG	GACGGCCGAC	AACGCCGGGG	780
AAGAGGGGGG	CGAGGCTCCC	CAGGAGCCCC	AGAGCTGAGT	GTTGCCCGCC	ACCGCCCCGC	840
CCTGCCCCCT	CCAGTCCCCC	ACCCTGCCGA	GAGGACTAGT	ATGGGGTGGG	AGGCCCCACC	900
CTTCTCCCCT	AGGCGCTGTT	CTTGCTCCAA	AGGGCTCCGT	GGAGAGGGAC	TGGCAGAGCT	960
GAGGCCACCT	GGGGCTGGGG	ATCCCACTCT	TCTTGCAGCT	GTTGAGCGCA	CCTAACCCT	1020
GGTCATGCCC	CCACCCCTGC	TCTCCGCACC	CGCTTCCTCC	CGACCCAGG	ACCAGGCTAC	1080
TTCTCCCCTC	CTCTTGCCCTC	CCTCCTGCCC	CTGCTGCCTC	TGATCGTAGG	AATTGAGGAG	1140
TGTCCCGCCT	TGTGGCTGAG	AACTGGACAG	TGGCAGGGGC	TGGAGATGGG	TGTGTGTGTG	1200
TGTGTGTGTG	TGTGTGTGTG	CGCGCGCGCC	AGTGCAAGAC	CGAGACTGAG	GGAAAGCATG	1260
TCTGCTGGGT	GTGACCATGT	TTCCTCTCAA	TAAAGTTCCC	CTGTGACACT	CAAAAAAAAA	1320

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Arg	Ala	Ser	Leu	Ile	Gln	Lys	Ala	Lys	Leu	Ala	Glu	Gln	Ala
1				5				10						15	
Glu	Arg	Tyr	Glu	Asp	Met	Ala	Ala	Phe	Met	Lys	Gly	Ala	Val	Glu	Lys
			20					25					30		
Gly	Glu	Glu	Leu	Ser	Cys	Glu	Glu	Arg	Asn	Leu	Leu	Ser	Val	Ala	Tyr
			35					40					45		

Lys	Asn	Val	Val	Gly	Gly	Gln	Arg	Ala	Ala	Trp	Arg	Val	Leu	Ser	Ser
50						55					60				
Ile	Glu	Gln	Lys	Ser	Asn	Glu	Glu	Gly	Ser	Glu	Glu	Lys	Gly	Pro	Glu
65					70				75					80	
Val	Arg	Glu	Tyr	Arg	Glu	Lys	Val	Glu	Thr	Glu	Leu	Gln	Gly	Val	Cys
			85					90						95	
Asp	Thr	Val	Leu	Gly	Leu	Leu	Asp	Ser	His	Leu	Ile	Lys	Glu	Ala	Gly
		100					105						110		
Asp	Ala	Glu	Ser	Arg	Val	Phe	Tyr	Leu	Lys	Met	Lys	Gly	Asp	Tyr	Tyr
	115					120						125			
Arg	Tyr	Leu	Ala	Glu	Val	Ala	Thr	Gly	Asp	Asp	Lys	Lys	Arg	Ile	Ile
130					135						140				
Asp	Ser	Ala	Arg	Ser	Ala	Tyr	Gln	Glu	Ala	Met	Asp	Ile	Ser	Lys	Lys
145				150						155					160
Glu	Met	Pro	Pro	Thr	Asn	Pro	Ile	Arg	Leu	Gly	Leu	Ala	Leu	Asn	Phe
			165					170						175	
Ser	Val	Phe	His	Tyr	Glu	Ile	Ala	Asn	Ser	Pro	Glu	Glu	Ala	Ile	Ser
		180					185						190		
Leu	Ala	Lys	Thr	Thr	Phe	Asp	Glu	Ala	Met	Ala	Asp	Leu	His	Thr	Leu
	195					200						205			
Ser	Glu	Asp	Ser	Tyr	Lys	Asp	Ser	Thr	Leu	Ile	Met	Gln	Leu	Leu	Arg
210				215							220				
Asp	Asn	Leu	Thr	Leu	Trp	Thr	Ala	Asp	Asn	Ala	Gly	Glu	Glu	Gly	Gly
225				230					235						240
Glu	Ala	Pro	Gln	Glu	Pro	Gln	Ser								
			245												

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCCAGC	CTGCCCCTCC	ACTTCTCTCC	CAAGCCAGGT	CCCGGCATGG	GTGGGTTATG	60
CTCATGCTGG	CAATACTTGA	AACGGGTTTA	TTAATGCTGG	GTATTTTGCA	CAATTTTATA	120
GACCTCTTTT	CTACATAGTC	TTTTTTAAAT	GGAAGGAGAA	AATGTCAGCC	ACATTACTGT	180
CTGTGTAGTG	CCAGGTGAAG	GGTTATCAGA	AGGCTGGTTG	GTTTAAATAA	GTTTATTCCA	240
AGAGACCTTC	TGGCTGGAAT	GAGTGAGAGT	GTGTGTGCAT	GTGTGTGTGT	GTTTCATGTGT	300
GCCCTGTATG	AATGTGGCTG	GCTCCCAGAT	CCCCTGGGCT	GCCCCCTGCC	CCATCCCCTT	360
TGAGTATCAG	AAGCACTCTG	AGCCAAGGGG	ACAGGGGGCA	CGTGCACTGG	TCACGAGAAA	420
ACCCTGGGCT	CCCACTGGGG	CTCAGCCCAG	CCTCCTATCT	TTCCTTCTTC	TATGGACTTC	480
AGACAGCCAG	TGTCTGGGGA	CTCTGCCACT	CTACCCCCAG	CCCTACCCAC	CAGCCCCCAG	540
GTGAGGCTTC	CAGCTGGGAC	CTGCCCAGAC	AGGCTGAGCC	TGGGCGTGGT	GGGTGGGGTG	600
ATGGCTCTGG	GGAGCGGCTG	CCATCCTACA	AGCCACACCC	CCTCCTCTGA	GCTCTGAATA	660
TGGGACCCAG	TGCCAGGAGC	TGGAAGACAA	GGTGTCTCTG	CCAAACGGGA	CCTCCATCCA	720
GAGAAAAGGA	AGAAGGTGCA	GGGTGGGCCA	AGAGGCAAGT	GAAGGTGGGC	CTGAGTCTGG	780
GCCGGAAACT	CAGAGGATGT	TTCTCCTCTG	CTGGGAGCTG	TAGTTTCTTA	TCAAATAGA	840

TATTGTTCCA	CCATCCCCCT	CCTTGGCCCT	TCAAGTGGGC	TGAAGCCTTG	GAAAGTGACA	900
TAGGAAGTCC	CCAGATCTTG	CCCTTCTCAC	TCCAGAGGCT	AGTGGTCACA	GACAGCTGGG	960
AATGGCAGCC	ACAGAGGGTC	CCTCTGGAGA	AACAGCTTCA	CCCCAGCCTC	AGGGCCCTGG	1020
GCATCACTGC	AGTGGCCCTG	GGAGGTGAGG	AAGAAGCTGG	CTAGAGGAGG	GGGCTCCCAC	1080
CTACCTTTTA	TTTAAGCCAG	TATTCTTTGT	TCCTGCTTGT	AATAAACTT	CAGTTTATAA	1140
GAGTTGCTTT	GCTTTGGTTT	GGTTTTTGTT	TGCTTTTCCT	TTGCTGAGGC	CCCAACTGGG	1200
AGCCCTCTGT	TCTTTCAGAC	AAATTTGGTT	CTTTCCTGGG	GAGACTGTGA	GAAGGCAGGC	1260
AGCCCAGTGA	TCTGGCTACA	TTTTCCCTCA	CCTGGCTGGA	GCTCTGTCCG	CTGGAGGAAG	1320
AGCAGAGAGG	GCTGCGGCTG	AGCCCCCATG	GGCACGTGAA	AAGAGGCCAT	CCTGTCCCCT	1380
CTTTGTCCCC	TCCACCTTCC	CCTGCCTCAG	GGGCTTGGAG	ACCCCAAATT	CTTCTTCCCT	1440
ACTGCCTTTC	CACTCCGATC	CCCAATGAGT	GCCCAGCTAA	GAAAATGTTT	GAGACAGTAG	1500
ATTCCAGTTT	GAGAGCCGGA	GCTTCCCTGG	CTACCACCTC	CAACCTGGGC	ACCAGGGCCC	1560
AGCCAGACAA	CCATAACAC	TGGCCCCACT	CTCTGGTATC	TCCCTCAGGA	GGACACCTGT	1620
CAGGATTTTG	CCTATCTCCTG	CACAGCCTGA	GGGGAGCTAA	CAGGCCCTCT	TGCAGAGGGT	1680
TAGCTGGTAA	GACCGTTTCT	TCCCTGTGCG	CCAGCACTGC	CCGCTCCCCT	CCACACACCA	1740
TCTCATCCTC	ATCGCATGCC	TCGCCAACCC	CATGGAGCCC	GTCCATCTGT	CTGGTGTGTG	1800
GTGCGGTGTG	TGTGCTGGTG	GTGGTAGGGT	CTCCAGGGAC	TCCCCGCTAA	GCAGAAGGAT	1860
CGGGATATAG	GGCAAGGCTA	AAAGCCCAGC	CCCATTGTGG	ACTGAGGAAG	TACGTTCCGG	1920
CAGAGCAGCT	CTCCAGCTGG	AAGAGGAGGT	GGAGGGTGAG	GCTGGGGAGA	GGATGGCGAA	1980
CCTGCCCTGA	GGTGCTTGGG	TCTGTGCTGG	TGGGGTCCTG	GTATGCAGGG	GCCACCGGTC	2040
ACTAACACTC	TTATGTCCTG	GCTTCTGTGC	CCCCTGAGC	TTTCTCTCAC	CCGCCCGTTT	2100
TCTCTCCTGC	TTCATTGCCT	GCTGCCTAAG	CCTTGGCCCT	TCTCTCGGGC	AGAGGCAGGT	2160
GCTGTGGCAG	CACCTCTCCC	CACCACCGGG	CCCCTGCAGG	CCGCCTCCCT	CCTCCCAGGC	2220
CTGCTAACCC	TCTCTCTTCT	CCTTCTTTTG	TGTCTGCGCG	GGGATCTCCA	GTGTGTGCGG	2280
GGGCTTAAGG	ACCTCCTGAG	GACCGCTGCT	CTCTGCCTCT	CCAGGAATGG	CCTGGGGGGA	2340
GCCAGGCACC	CGGCACCTCC	ACCTGCCTAA	CCTGTGGCCC	ATCTGCCACC	ATCTGTGCCT	2400
ACAGGGTCTG	CCCCCAGCC	TGCCCCGCCT	GTGTGCTCTC	TAGGACCCCA	TAGGGGGCAG	2460
GGGCTGGCCT	CTTTGCCCCA	TTCCCGCTCC	ATGCCGGCCA	GAGTGATAGAA	AGCCATAACG	2520
CACGCAGCCA	TCAGCACAA	AATGTGACTC	TACGCTGATA	TGCTCCCTCT	CTCCTCCACT	2580
GACTTCCCCCT	TCCCGGATTT	GTGAGGTGTC	AAGACTAGGA	ATCTGGCCTT	AGAGCCTGCC	2640
CCTCCACCCC	CTCAGATCAG	GCATAGCCAT	AGTCAAGCCC	AGCAGGTTTC	CTCAGGAGCT	2700
GTCTGGGGTG	TTGATGGTGG	ATGACGCTGC	TGAACAAGTT	TGGTGACTGT	TCTAAGCACA	2760
ACTGGCTTGA	TACTGTTCCC	ACGGCCTGTC	CACCTCCCAC	CCCCAACCCCT	CCACCAGAGT	2820
AGGTAGGATG	TAGGGAGGGT	GCGTGCCGCG	TTTGCTCTAG	GCACTGAGGG	ACCAAGCTAG	2880
CCGTGCACAG	CCCCATACAC	TTCAGGGGCG	TAAAGGAAG	AGCTGAGCCA	AGGAAAATCA	2940
GCTAGGCCCC	GGGCTGGGGG	CTGCTTGTCT	GCTATCCTGT	ACCTTTTFTT	TTTTTAACCA	3000
AAATAAAGAT	TCCCCTCTTC	TTGCCATACC	ATTGGCTGTC	TGGTGGCGCC	TTTACTTTGG	3060
GGCCCAGGGA	TGGGACCTGC	AGTGGGCGTG	TGGAACATAT	GGCTCCCCCT	CGCTCCCAGC	3120
TTTCTTCCAG	CTGGCCAGTG	CTGCTCTGGA	GATTTACAAG	CACAACGAAG	CCAGGAGGGA	3180
CACAGGAAAA	GTGGCTGACA	TCCTTTTCAC	TCTGCCCCCT	CAGAACTCTT	GGTCTCAATT	3240
CCAGACACCA	CCCAGCCTTA	GCTGACCTCT	GGATTCTGAT	AGGTCCCAGT	GCAGGCTGAG	3300
ACAGAGGGTT	TAACTCCAGT	TTGGGACTGC	CATACCCATG	AACTGAGCCC	AGCCCAGGGT	3360
AACGATCTCA	TGGAAACTTC	TCTCTCCCCA	GTTGCTGCAC	TACATCAAGA	TACACACATG	3420
TGCATACACT	GTAATATGGG	CTAAAAAAT	ACGTACCGCT	ACCGTTCAGC	AAGGGCTTGC	3480
CGAGTCCCGG	GCCCATTTTC	TCATCTTAAC	CTGTGAGGAG	GATGATGTCA	GCCTTTTAC	3540
AGATGAGGGA	ACTGAGACTC	AAGGAAGAAA	CAGGAGCTGC	CCAAGGTCAC	CCAGCTGGCA	3600
AAGCAGCAAA	TCCCAGATCG	GAACCTGATC	TCTGCCCCGA	GCTCTGAGCC	ATCTGCACTA	3660
CCCAAGGAAT	GAATACAGCG	GTGGGAGGAT	GAGATCTTGG	AGAAAACCTA	AAATTAGAGA	3720
ATGTCATAGC	CAGTAGAGGG	CTTAGAGTTG	ATCTGGGCCA	GCCTCCTTGT	TTTACTGATG	3780
GAGAAATTGA	AGCCCAGAGG	CAGGAAGGGA	CCTGCCCAAG	GCCTTATAAC	AGAGCTGGGA	3840
TGCAGTCCCA	CACTCTGACC	TCATTCCATT	CTCTCTCCAT	AAATTCTGCA	CTGTCTCTAG	3900
ACTGGACTGG	TTTAGATGTG	GGATACTCTA	AACAGCAGTG	CCTTCAAGAG	AAAAAGAATC	3960

AGAACTACGA	ATCACTTAAA	AGTAATGTAA	GCTACTCTGG	GCACACTGCC	TATGGGGTCG	4020
CCCTGCTCCA	CAAGGAGCCA	CAAAAATAAT	TAAAAATAATT	TAATATCCCT	TCCCAAAGGT	4080
AACCAGTAAA	GTAAGCTCTT	GGCTAGGTAA	CTGGACTCTT	GTTCACTACT	AGCCAGTGGG	4140
AAAAGGTGCT	AGAGCTTCCT	CTGGCCACCT	GTTTAATTTG	ATCATTCCAA	GACAGAAACA	4200
TTTCTTAGGA	AGTTCTTTCT	AGAATCTACC	TGGTGTCCCT	CCCCTGCTA	TCAGAGCCCT	4260
GTCCTCTGTC	CTCAGTGGAG	GTAGAGAGCA	AATGGTTGCT	GCTTTCTTCA	TCACAACCCT	4320
TCAAAGCCTA	TTATTACCAG	CTAAGAAGGA	TTGGTTGACT	ATGGGCCAGA	GCCCCGTGAGC	4380
CTGCTGGTAG	AATGGATGCT	GTACAGGAGG	GTGGGGAGGT	AGCAGGCAGA	ATGAGGAAAG	4440
CCCCTTTGAG	CTGCAACCCC	AGCTCCTGTC	CTGCTGACTC	AGACAGCTGA	CTGTGGAGCT	4500
CCATGCCCTG	CCAGGGCCTG	CTGCCTCCTG	CCCGTCTGAG	CTCCTGAACT	TGGGAAATGG	4560
AGGCCCAGAG	GCAAAGGGAG	GTACCTGAGA	CAGGAATCTG	GTCAGGATCA	ACAGGCCAGA	4620
GCGGGCAGGA	GGTATCAGGC	AGCCTGGCTC	CCAGATGCAC	CCCTGAGCTC	CAGCAGGGGA	4680
GGAGTAGGAA	TGAAGGGGCT	TCCTTGCCCT	TGCTCATGGC	TATGCGGAGG	GCGTGAACCA	4740
CCACCAGGTC	CTCTGGCTTA	AGTGGCGGGA	AGCAAATGGT	CCCTCCCTGG	ACTCAGGCTC	4800
CAAAGTTCCT	GGGCCTGCCT	TCCAGGTTCC	CAGTGTCTCTG	GGATCTCCAG	CTTTCCCCAG	4860
GACTTGGGGA	AGCCCCGGCT	GGATGACTAG	TACAAATGAA	GGCCCCCTGAG	GTTCCAGGAC	4920
CTGCTGAGGT	CACAGGAATA	TCCTAGATCA	AGCTTGTCCA	ACCCACGGCC	CACAGGCTGC	4980
ATGTGGCCCA	GAATGGCTTT	GAATGCAGCC	CAACACAAAT	TAGTAAACTT	TCTTAAACA	5040
TTATGAGATT	TTTTTGCAA	TTTTTTTTTTT	TTTTTTAGCT	CATCAGTTAT	TGGTAGTGTT	5100
GGTATATTTT	ATGTGTGGCC	CAAGACAATT	CTTCCAATGT	GGCCCAGGGA	AGCCAAAAGA	5160
TTGGACACGC	CTGTCCTAGA	TGGAGAGGAA	GGAGGCAGTG	CTGAGCACAT	CTGGCCATTC	5220
ATCCATCTGG	AGAGAGAAGG	CTATGGGCAA	ACTGCTTCCT	CTCCCCGTGA	GACACCCAGC	5280
TGGGAAGGTC	TGGCCTTTGG	TAAGTCCTGG	CTTGGGGTCC	TTCTCATTTT	CACAGAACCT	5340
AACTCTATGT	TAGTGCTTTG	TGAGTATATG	TTGATCATAA	TAAAGTTGAC	GGGATTTTTT	5400
CACATGATAA	TAATAGTTGT	CATCTGGCCG	GGCATGGTGG	CTTATGCCTA	TAATTTTCAGC	5460
ACTTTGGAAG	GCTGAGGCAG	GTGGATCACT	TGAGGTCAGC	TGTTGAGAC	CAGCCTGGCC	5520
AACATGGTGA	AACCACATCT	CTACTTAAAA	AAAAAAAAAA	TACAAAAATT	AGCTGGGTGT	5580
GGTGGTGCAC	CCTTGTAATC	CCAGCTACTC	GGGAGGCTGA	GGCAGGAGAA	TCACTTGAAC	5640
CCAGGAGGTG	GAGGTTGCAG	TGAGCTGAGA	TTGTGCCACT	ACACTCCAGC	CTGGGTGACA	5700
AGAGCGAAAC	TCCGTCTCAA	AAAAAAAGAA	AATAATAATA	ATAATAGTTG	CCATCCATTC	5760
TACTGTGCTT	TCCATTAAC	CGTGTAAATCC	TCACAAGTCC	CATTTTATAG	TTACAGGAAC	5820
TGAGGCTCAC	AGAGCTTAAA	TCACTTGGCC	AAGGCCACAA	ACAGCTATAA	GAATTACATT	5880
TAGGCAGTCT	GATTCCAAAG	ATACTAGTCT	ATTCTGTATC	TCATAGACAA	ACAATACATA	5940
TTCACTTTTT	TGTTTGTGTT	TTGTTTTGAG	ACGGAGCTTT	GCTCTGTCAC	CCAGGCTGGA	6000
GTGCAGTGGC	GCCATCTCGG	CTCACTGCAA	CGTCCGCCTC	CCGGGTTCAA	GCGATTCTCC	6060
TGCCTCAGCC	TCCCGAGTAG	CTGGGACTAC	AGGCATGTGC	CACCATGCCC	GGCTAATTTT	6120
TTGTATTTTT	AGTAGAGACA	GGGTTTTTCT	GGGTTAGCCA	GAATGGTCTC	GATCTCCTGA	6180
CCTTGTGATC	CACCCACCTC	AGCCTCCCCA	AGTGTGAGA	TGACAGGCGT	GAGCCACCGC	6240
GTCCGACCTA	TATTCATAT	TTATAAATTG	GAGAGAATAA	GAAAATCAAA	AGGGCCAGGT	6300
GTAGTGAATC	ACACCTGTAA	TCCCAGCACT	TTGGGAAGCC	AAGGCAGGAG	GATTGCTTGA	6360
ACCCAGAAGT	TCGAGACCAG	CCTGGGCAAC	ATGGTGAGAC	CCTGTCTCTA	CAAAAAATAC	6420
AAAAATTAGC	TGGGCGTTGT	GGTGAGCACC	TTATTCTTAG	GAAGCTGAGG	CAGGAGGATC	6480
ACCTGAGGCC	AAGGAGGTTG	AGACTGCAGT	GAGCTGTGAT	CATACCACTG	TACTTCAGCC	6540
TGGACATCAG	AGTAAGACCC	TATCTCTAAA	AAGGAAATTG	AGAAGAAAGA	AAATCAAAGG	6600
GAAGCAAAAT	CACCTACTCT	CACCTACCTA	AGATACCCCT	TAGAAGTTGG	TATTTTAGTG	6660
TGGTTCCTAT	TGTTTTCTGT	GTCAGTTCTC	TGATTTGAGC	AAAATCTTTG	GGACGTCAAA	6720
CTTAAAAATCC	CCTTTACTTC	CTTGGAACCC	CTGTAGCATT	AGCCCAGACA	TGTCCCTACT	6780
CCTCCTTGTC	GCAAAGAGAA	GGATCTCGTC	TTTGGTCCCC	AGAGTTCTGG	CCTAAGCCTC	6840
CCTCCAGGAG	GGAAGATGAG	TGTTTCAGACA	CTCAGAGTAG	CTGGGGGAGA	CACAGGCTTG	6900
TGAAATTATC	CTGGCTCAAC	TATTAGGTCG	GCAGAATCCC	AGTGAAGGGA	GCCCTACCTC	6960
TGAGCCCCAT	CTAAGCTTTG	GCTATGGGTG	GGGCAGATAA	GCAGGAATCC	ATCCCTATAG	7020
GCTCAATGCC	AACACCCTTA	GGTGAAACTC	TTGATGAAAC	TTGAGGCCAG	GGCTCCGGCA	7080

AGCAGGGAAA	GAACGTTGGC	AACAGAGGTC	TCCATCTCTG	AGGACTCTGC	CAGGGGTCAG	7140
AGATGGGGCA	ATGGTCAAAA	GGAAGGAACA	GGCCAGGCAC	AGTGGCTCAT	GCCCATAATC	7200
CCAGCACTTT	GGGAGGCTGA	GGCAGGAGGA	TCGCTTGAGC	CCAGGAGTTT	GAGACCTGCC	7260
TGGGCAATGT	AGTGAGATCT	GCTCTCTATT	TAAAAAAAAA	AAAAAGGAAA	GAACAAGTAA	7320
ACTTCTGAGA	AACAGGCTGG	GGGAGGCATC	ACGTAGCTGG	AATTGCTGCC	CCATAAAACA	7380
GAATGGTATG	TGTCACTGCC	ACCTCCCTTT	CTCAGTCCTC	TCTCTCCCCA	GGTTGCTAGC	7440
GTCCCCCTGG	GGGATCAAAC	TGGACTGCTT	CCCAGCCTCA	GACAGAGAGC	AGTCTGAGTC	7500
AGGCAGGAAA	GTGGGACAGC	CGGGGAGCTG	GACCCCAACC	TCTGTGAGCC	CCGCTGGTAC	7560
CTGATGGCAT	GTGGCTTGGA	GAGGGCAGGT	GACCTGGCGT	GGAGGGCCAG	AGGGTAAATC	7620
CTCAAACAAG	TGGCAACAGG	CCACCAACTT	GAAAGGGAAA	ATTGTGTAGT	GATGGGAAAT	7680

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGCATGTGC CACCATGCCC

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTAGCATTAG CCCAGACATG TCC

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